

1

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<212> PRT

<213> Homo sapiens

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- Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val 35 40 45
- Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val 50 55 60
- Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr 65 70 75 80
- Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu 85 90 95
- Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe 100 105 110
- Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
  115 120 125
- Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg 130 135 140
- Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg 145 150 155 160
- Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu 165 170 175
- Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe 180 185 190
- Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
  195 200 205
- Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe 210 215 220
- Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala 225 230 235 240
- Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala 245 250 255
- Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val 260 265 270
- Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg 275 280 285
- Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val 290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser 305 Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala 330 Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu 355 Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu 385 390 395 Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr 405 <210> 3 <211> 1658 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (64)..(1299) <223> IGS4A short version <400> 3 ggctcagctt gaaacagagc ctcgtaccag gggaggctca ggccttggat tttaatgtca 60 ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta 108 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu 1 5 10 gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156 Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala 20 ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204 Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val 35 gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252 Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val 50

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														ctt Leu		348
														ttg Leu 110	Phe	396
														gtg Val		444
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Gly 999	tcc Ser	ctg Leu	gtc Val 195	cca Pro	ggt Gly	tcg Ser	gcc Ala	acc Thr 200	tgt Cys	acg Thr	gtc Val	atc Ile	aag Lys 205	ccc Pro	atg Met	684
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caagaacgtg actgga	aagg catggcacct	t ataccttgat	taatttccat taatggaaat	1609
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<211> 412

<212> PRT

<213> Homo sapiens

<400> 4

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Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala Phe 20 25 30

Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val Val 35 40 45

Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys
50 55 60

Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr 65 75 80

Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Gly Met 85 90 95

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly 100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe 115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala 130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Ala 145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu 165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly 180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp 195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu 210 215 220

Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu 225 230 235 240

Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile Gln 245 250 255

Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val Leu 260 265 270

Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe Phe 275 280 285

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Pro	Ile	Ile	Tyr	Asn 325	Leu	Leu	Ser	Arg	Arg 330	Phe	Gln	Ala	Ala	Phe 335	Gln	
Asn	Val	Ile	Ser 340	Ser	Phe	His	Lys	Gln 345	Trp	His	Ser	Gln	His 350	Asp	Pro	
Gln	Leu	Pro 355	Pro	Ala	Gln	Arg	Asn 360	Ile	Phe	Leu	Thr	Glu 365	Cys	His	Phe	
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Arg	Ala	Leu	Arg 165	Ile	Leu	Gly	Ile	Val 170	Trp	Gly	Phe	Ser	Val 175	ctc Leu	Phe	585
Ser	Leu	Pro 180	Asn	Thr	Ser	Ile	His 185	Gly	Ile	Lys	Phe	His 190	Tyr	ttc Phe	Pro	633
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		aga Arg														1299
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<211> 415

<212> PRT

<213> Homo sapiens

<400> 6

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Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
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Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val 35 40 45

Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
50 55 60

Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr 65 70 75 80

Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu 85 90 95

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe 100 105 110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr 115 120 125

Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg 130 135 140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg 145 150 155 160

Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu 165 170 175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe 180 185 190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
195 200 205

Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe 210 215 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala 225 230 235 240

Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala 245 250 255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val 265 Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg 280 Leu Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val 295 Phe Asn Leu Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser 310 315 Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala 330 Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln 345 350 His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu 360 Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys 375 380 Gln Ser Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu 400 Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr 410 <210> 7 <211> 1658 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (64)..(1299) <223> IGS4B short version <400> 7 ggctcagctt gaaacagagc ctcgtaccag gggaggctca ggccttggat tttaatgtca 60 ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa cta Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu

gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala

25

20

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													gtc Val			252
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													ctc Leu			348
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Gly 999	ccc Pro	gtg Val	ggc Gly 115	tgc Cys	tac Tyr	ttc Phe	aag Lys	acg Thr 120	gcc Ala	ctc Leu	ttt Phe	gag Glu	acc Thr 125	gtg Val	tgc Cys	444
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35 40 45

Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys 50 55 60

Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr 65 75 80

Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Gly Met 85 90 95

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly 100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe 115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala 130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Ala 145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu 165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly 180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp 195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu 210 215 220

Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg Leu 225 230 235 240

Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val Leu 260 265 Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe Phe Ser Phe Val Glu Glu Trp Thr Glu Ser Leu Ala Ala Val Phe Asn Leu 290 295 Val His Val Val Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe Gln 330 Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His Phe 355 365 Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Leu Cys Gln Ser Ser Val His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln Met Ser 385 390 395 Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr 405 <210> 9 <211> 1594

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gtg Val	tgc Cys	ctg Leu	gtg Val	att Ile 70	ctg Leu	cag Gln	cac His	cag Gln	gct Ala 75	atg Met	aag Lys	acg Thr	ccc Pro	acc Thr 80	aac Asn	297
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cgg Arg	gcc Ala	ctc Leu	agg Arg 165	atc Ile	ctc Leu	ggc Gly	atc Ile	gtc Val 170	tgg Trp	ggc Gly	ttc Phe	tcc Ser	gtg Val 175	ctc Leu	ttc Phe	585
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atg Met 210	tgg Trp	atc Ile	tac Tyr	aat Asn	ttc Phe 215	atc Ile	atc Ile	cag Gln	gtc Val	acc Thr 220	tcc Ser	ttc Phe	cta Leu	ttc Phe	tac Tyr 225	729

		Val Ile			Tyr Leu Me	g gca ctc t Ala Leu 240	777
				Ala Asp	gaa ggg aa Glu Gly As 25	n Ala Asn	825
	g Pro Cys				atg ctg tc Met Leu Se 270		873
					acc tcg tcc Thr Ser Sec 285		921
tgt cag gt Cys Gln Va 290				agc tgtca	aacccc atta	tctata	972
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- Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr 65 70 75 80
- Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu 85 90 95
- Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe 100 105 110
- Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr 115 120 125
- Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
- Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg 145 150 155 160
- Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu 165 170 175
- Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe 180 185 190
- Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys 195 200 205
- Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe 210 215 220
- Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala 225 230 235 240
- Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala 245 250 255
- Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu 260 265 270
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                                                                  108
    Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc
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Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
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ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg
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Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val
gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg
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Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val
tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac
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Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr
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Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Gly
atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc
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Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe
ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc
                                                                  444
Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys
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ttc gcc tcc atc ctc agc atc acc gtc agc gtg gag cgc tac gtg
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Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val
gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg
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Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
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ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga 78 Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg 225 230 235	30
cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att 82 Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile 240 255	28
caa aga ccc tgc aga aaa tca gtc aac aag atg ctg tct ttg tgg agg 87 Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg 260 265 270	16
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Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val Cys 50 55 60

Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr Tyr 65 70 75 80

Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Gly Met 85 90 95

Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe Gly 100 105 110

Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys Phe 115 120 125

Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val Ala 130 135 140

Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg Ala 145 150 155 160

Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser Leu 165 170 175

Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn Gly 180 185 190

Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met Trp 195 200 205

Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu Leu 210 215 220

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Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Ser Leu Trp Arg Ser
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<223> Description of Artificial Sequence: Synthetic
      primer
<400> 33
ggaggcgaag cacacggtct ca
                                                                    22
```

```
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<220>
<221> misc_binding
<222> (1)
<223> Labeled with 6-carboxyfluorescein
<220>
<221> misc_binding
<222> (34)
<223> Labeled with
      N, N, N', N'-tetramethyl-6-carboxyrhodamin
<400> 34
agatgtggcg caactaccct ttcttgttcg ggcc
<210> 35
<211> 7
<212> PRT
<213> Unknown Organism
<220>
<223> Description of Unknown Organism: Illustrative
      mammalian C-terminal sequence
<220>
<223> C-term amidated
<400> 35
Phe Leu Phe Arg Pro Arg Asn
 1
                  5
```

34

<210> 34